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Multivariate analysis and its implication in breeding of desired plant type in garden pea *(Pisum sativum)*

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ABSTRACT

Genetic variance was evaluated in one hundred sixty genotypes of garden pea (*Pisum sativum* L.) for nine morphological traits through multivariate analysis. Analysis of variance indicated that the genotypes varied significantly among themselves in respect of 9 characters studied. The genotypes were grouped into 14 clusters depending upon their morphological similarity through principal component analysis. Clustering pattern indicated that majority of genotypes, i.e. 113 (70%) were genetically close to each other and grouped in 3 clusters, while apparent diversity was mainly noticed due to 47 genotypes (30%) distributed over 11 clusters. The maximum inter-cluster distance was noticed between III and XIV (61.49) followed by III and VII (51.33) and III and XII (53.27). Considering cluster mean, the genotypes of cluster III might be selected as a suitable parent for future hybridization programme. The contribution of each character towards the expression of genetic divergence indicated that 10-pod weight contributed maximum (58.29) followed by days to 50% flowering (23.83), plant height (11.31) and shelling percent (4.95%). These four characters contributed more than 98% to the total genetic divergence in the genotypes studied.

Key words: Canonical vector, Cluster pattern, Garden pea, Hybridization, Multivariate analysis

Garden pea (*Pisum sativum* L.) is an important vegetable grown throughout the world. As a cool season crop, it is extensively grown in temperate zone; but restricted to cooler altitudes in the tropics and winter season in the subtropics. A rich source of digestible proteins (7%), amino acids and sugars (12%), green peas are an all-time favourite vegetable. India is the leading pea producing country in the world. During 2012-13, it is grown in about 0.42 million ha area producing 4.01 million tonnes with productivity of 9.5 tonnes/ha (Anonymous 2013). It is extensively grown in Uttar Pradesh, Madhya Pradesh, Jharkhand, Himachal Pradesh, Punjab, West Bengal, Haryana and Bihar contributing to 90% of the total production of India.

Genetic diversity is very important factor for any hybridization program aiming at genetic improvement of yield especially in self-pollinated crops. To breed desired plant type, information about germplasm diversity and genetic relatedness among elite breeding material is a fundamental element in plant breeding. For creating variability, crossing among parental lines is the most potent and assured method. However, selection of divergent parent is most important, as greater the genetic divergence among the parents for the characters; better are the chances of releasing the variability (Singh 1991). Genetic study based on the multivariate analysis is a powerful tool for determining the degree of divergence between populations, the relative contribution of different components to the total divergence and the nature of forces operating at different levels (Ceolin *et al.* 2007). Hence, the present study was undertaken to study the nature and magnitude of genetic divergence, to identify characters which contribute maximum to genetic diversity and to identify suitable genotypes for use in breeding programme for broadening the genetic base in garden pea.

MATERIALS AND METHODS

A total of 160 genotypes of pea collected from different parts of India were grown in a completely randomized block design replicated thrice at research farm of the ICAR-Indian Institute of Vegetable Research, Varanasi. The plot for each genotype consisted of 5 rows of 3 m length spaced at 30 cm; while the plants were spaced at 5 cm distance. The crop was sown in first week of November 2011 and followed recommended cultural practices to raise a good crop. Field observation were recorded for plant height (cm), days to 50% flowering, first pod node number, pod length (cm), number of pods/plant, number of seeds/pod, 10 pod weight (g), pod yield/plant (g) and shelling per cent. Ten competitive plants were randomly selected from the central

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row of each plot in each replication to record observations on the quantitative traits. The statistical analysis was done on the mean basis across the genotypes. The difference among population was tested by analysis of variance for individual traits and by Wilk's lambda criterion for pooled effect of all the 10 characters. D^2 analysis was done following Rao (1952) to determine degree of differentiation among n(n-1)/2 pairs of 'n' population. Grouping of genotypes was done according to Tocher's method (Rao 1952).

RESULTS AND DISCUSSION

Analysis of variance (Table 1) indicated that the genotypes varied significantly among themselves in respect of 9 characters studied. The analysis of plot means revealed significant differences among 160 genotypes for each of nine characters suggesting appreciable variability among the genotypes. The simultaneous testing of significance based on Wilk's (Lambda) criterion also showed significant differences among cultivars for aggregate of all the characters. The D^2 values estimated for 160 germplasm lines in n(n-1)/2 = 12720 combinations varied from 0.63 to 4204.83 indicating the presence of substantial amount of genetic diversity in the population. The 160 genotypes were grouped into 14 clusters depending upon their morphological similarity (Table 2). Among these, cluster I was the largest having 45 genotypes, followed by cluster IV with 35 genotypes and cluster II with 33 genotypes. Clusters VI, III, and V contained 19, 12 and 8 genotypes, respectively. From cluster VII to XIV each had single genotype. Clustering pattern indicated that majority of genotypes, i.e. 113 (70%) were genetically close to each other and grouped in 3 clusters, while apparent diversity was mainly noticed due to 47 genotypes (30%) distributed over 11 clusters. The genotypes involved in clustering are group of Indian land races, improved varieties, exotic collections and selections obtained through different

Table 1 Analysis of variance (Mean sum of squares) for different characters

Trait	Abbre-viation	Repli-cation	Treatment	Error
	DF	2	159	318
Plant height (cm)	PH	3.91	40.25**	11.18
Days to 50% flowering	DF	58.96	528.30**	0.99
Number of node for first pod	IFP	0.05	23.52**	0.36
Pod length (cm)	PL	0.12	3.78**	0.19
Number of pods per plant	NPP	11.54	53.32**	1.49
Ten pod weight (g)	TPW	220.91	1058.39**	0.75
Number of seed/pod	NSP	1.93	3.32**	0.54
Pod yield/plant (g)	PYP	758.24	1168.02**	46.46
Shelling percent	SP	69.89	76.72**	0.91

*Significant at 5% level of probability, **Significant at 1% level of probability. PH-Plant height, DF-Days to 50% flowering, IFP-Number of internodes for first pod, PL- Pod length, NPP-Number of pods/plant, TPW- Ten pod weight, NSP- Number of seeds/pod, PYP- Pod yield/plant, SP- Shelling percent

Table 2 Composition of different clusters in pea

Cluster	Number of genotypes	Name of genotypes
I	45	AP-1, VRP-263, VL-7, VRP-313, VRMP-7, VRP-401, KS-205, VRPM-5, VRP-324, VRP-316, VRP-343, VRP-105 , VRP-102, VRP-337, VRP-387, VRP-216, VRP-315, VRPM-6, EC-9122, VRP-311, VRP-174, DHVP-10, VRP-165, Pusa Pragati, VRPR-10, VRP-139, VRP-154, VRP-204, VRP-62, VRPM-11, KS-228, NDVP-8, VRP-90, VRP-221 , PM-65, VRP-361, VRP-138, VRPM-2, VRP-305, VRP-360 , VRP-375, VRP-3, VRP-332, VRPMR-10, VL-03.
II	33	VRPE-27, VRPE-33, VRPE-52, VRPE-43, VRPE-33-1, VRPE-58, VRPE-45, VRPE-55, VRPE-2, VRPE-36, VRPE-21, VRPE-19, VRPE-54, VRPE-62, VRPE-11, VRPE-21-1, VRPE-29, VRPE-18, VRPE-28, VRPE-19, VRPE-81, VRPE-32, VRPE-25, VRPE-57, VRPE-30, LINCON, DPP-94-14, VRPE-6, VRPE-20, VRPE-38, VRPE-49, VRPE-64, VRPE-69.
III	12	VRPE-56, VRPE-21-2, VRPE-25-1, VRPE-39, VRPE-13, NDVP-1, VRPE-14, VRPE-60, VRPM-21, VRPE-28, PMR-53, DPP-9418-06.
IV	35	VRMPR-7, VRPR-2, VRP-156, VRP-13,VRP-162,VRP-322, VRP-77, EC-414482, KTP-8, VRP-355, VRP-339, DVP-8, VRP-143, VRPR-4, Shihar Local,VP-106, VRP-231, CHPMR-1, VRP-321, VRP-221, KS-245, VRP-205, VRP-266, VRP-258,VRPM-1, VRP-83, VRP-288-1, Macoimubi, SR-71, KTP-04,VRP-152, VP-215,VRPR-3,VRP-7, VRPM-10.
V	8	VRPE-17, DARL-407, VRPE-72, VRP-216, VRPE-31, VRPE-45, VRPE-24, VRP-212.
VI	19	VRP-306, VRP-13, VRP-111, VRP-387, VRP-129, PC-531, VRPM-5, NDVP-10, VRPE-2, VRP-292, VRP-8, VRPM-X, VRP-114, VRP-103, VRPM-15, NDVP-12, VRPR-15, VL-8, VRP-287.
VII	1	EC-97280
VIII	1	Arka Ajeet
IX	1	VRP-48
X	1	EC-71944
XI	1	DCP-2
XII	1	VRP-200
XIII	1	VRP-288
XIV	1	VRP-358

breeding programmes at ICAR-Indian Institute of Vegetable Research, Varanasi for the last two decades. The clustering pattern was also confirmed by spatial distribution of genotypes under canonical analysis. The distribution pattern of genotypes of diverse origin in a single cluster indicates that the geographical origin in pea was not related to genetic divergence (Kumar *et al.* 2007). The tendency of genotypes occurring in clusters cutting across the geographical boundaries demonstrates that geographical isolation need not necessary be related to genetic diversity and was at random (Gatti *et al.* 2011 and Kumar *et al.* 2007). This means that geographical diversity though important may not be factor in determining genetic divergence. The genotypes originating from one place as in present study were scattered in to fourteen clusters. Such parallelism between geographical distribution and genetic diversity might be due to some forces other than geographical distance like genetic architecture of population, heterogeneity, history of selection, proximity of development of traits etc. (Sureja and Sharma 2001).

The intra cluster value was found to vary from 0.0 to 15.94 (Table 3), the maximum being in cluster VI (15.94) followed by IV (13.84) and V (13.66). Sharma *et al.* (2013) also observed maximum intra-cluster variation among genotypes in their studies.The maximum inter-cluster distance was noticed between III and XIV (61.49), followed by III and VII (56.58) and III and XII (53.27). This indicates that the genotypes of these clusters are much diverse to each other. The magnitude of heterosis largely depends on degree of diversity in the parental lines, the higher distance between two clusters, the greater genetic diversity between genotypes. The crosses involving the diverse genotypes would be expected to manifest maximum heterosis and release of desirable transgressive segregants (Singh and Mishra 2008 and Nisar *et al.* 2008).

The diversity present in the material was also supported by the appreciable amount of variation among cluster means for different characters. Germplasm accessions in clusters II, III, and V were the earliest in days to flowering, whereas those in clusters IX and XI

Table 3 Intra (bold) and inter cluster distance (D^2) in pea

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
I	**10.20**	23.00	33.93	15.99	17.19	19.42	25.65	27.07	18.08	25.04	24.23	19.83	29.29	32.05
II		**9.41**	16.22	33.11	19.27	22.81	45.20	41.52	34.84	41.92	39.26	31.45	43.84	51.12
III			**8.52**	43.85	30.98	28.08	56.58	51.43	44.41	50.95	47.50	39.70	53.27	61.49
IV				**13.84**	24.96	25.91	17.28	17.47	16.37	19.02	22.25	20.49	24.55	23.62
V					**13.66**	25.97	34.60	33.91	28.72	34.47	34.21	27.30	36.75	41.79
VI						**15.94**	36.68	32.01	24.43	31.10	27.51	23.95	36.72	40.60
VII							**0.00**	14.14	19.98	17.41	24.78	27.32	23.07	13.47
VIII								**0.00**	24.14	10.86	28.95	17.33	11.25	11.68
IX									**0.00**	23.97	8.63	28.06	37.06	28.66
X										**0.00**	26.84	17.23	17.28	16.36
XI											**0.00**	33.16	39.43	32.58
XII												**0.00**	16.71	25.69
XIII													**0.00**	17.06
XIV														**0.00**

Table 4 Cluster mean for different characters in pea

Cluster	PH	DF	IFP	PL	NPP	TPW	NSP	PYP	SP
I	72.83	47.22	11.69	7.80	11.50	52.53	6.12	59.85	48.00
II	38.35	30.51	8.25	8.68	5.60	77.39	7.15	43.63	48.48
III	42.54	31.22	8.93	9.02	5.43	95.83	7.56	52.30	45.15
IV	98.37	55.72	11.43	6.76	13.13	40.84	5.44	53.21	48.24
V	33.52	30.29	7.60	7.84	5.48	55.00	6.10	29.62	45.00
VI	91.11	56.16	14.28	8.42	11.46	69.74	6.82	79.12	44.82
VII	116.50	64.00	10.83	4.58	13.00	23.33	5.45	30.22	51.33
VIII	177.33	59.00	10.50	6.42	13.17	35.00	5.72	46.15	51.00
IX	60.50	73.00	13.50	6.50	13.67	45.00	5.20	61.58	50.00
X	170.50	64.00	10.33	4.50	12.00	35.00	6.97	42.03	35.00
XI	56.00	85.00	11.33	8.08	10.83	45.00	5.60	48.65	45.00
XII	169.83	44.67	16.00	7.33	8.00	50.00	5.68	39.90	40.00
XIII	215.83	45.00	11.50	6.08	13.00	35.00	5.28	45.52	50.00
XIV	187.67	65.00	15.67	7.03	11.33	20.00	5.53	22.70	50.00

Abbreviation of traits provided in Table 1.

were of late type (Table 4). The genotypes in clusters IV, VI, VII, VIII, X, XII and XIV were tall type while bush type accessions were found in clusters V, II and III. The cluster III have highest number of seeds/pod (7.56), 10-pod weight (95.83 g), pod length (9.02 cm), lower number of internodes for first pod (8.93) and days to 50% flowering but had lowest number of pods/plant (5.43). The maximum pod yield/ plant (79.12 g) and third highest pod length (8.42 cm) as well as 10-pod weight (69.74 g) was noticed in cluster VI. Contrary to this, the cluster IX having single variety (VRP 48) was separated by other clusters due to highest number of pods/plant (13.67), second highest pod yield/plant (61.58 g) and third highest shelling per cent but accessions were late in maturity. The cluster XIV containing single genotype had lowest mean values for most of the characters. The cluster II had second lowest mean values of days to 50% flowering (30.51), number of internodes for first pod (8.25), second highest pod length (8.68 cm), 10-pod weight (77.39 g) and number of seeds/pod (7.15).

Considering vector analysis (Table 5), 10 pod weight (0.840), days to 50% flowering (0.389), plant height (0.269) and shelling percent (0.194) in first vector, days to 50% flowering (0.752), 10-pod weight (0.438), plant height (0.359) and number of nodes for first pod (0.237) in second vector and days to 50% flowering (0.449), plant height (0.869), pod length (0.101) and shelling percent (0.110) in third vector were noticed important contributor respectively to the total divergence. Out of total diversity, 93% was accounted by first 3 canonical roots and of these more than 87% was contributed by first two vectors (X + Y) suggesting that the differentiation for characters was nearly completed in three phases (Table 6). The analysis of the contribution of each character towards the expression of genetic divergence indicated that 10-pod weight contributed maximum (58.29%) followed by days to 50% flowering (23.83%), plant height (11.31%) and shelling percent (4.95%). These four characters contributed more than 98% to the total genetic divergence in the genotypes studied. Number of seeds/pod contributed nil to the total genetic divergence. On the other hand, earlier reports revealed that plant height (Kumar *et al.* 2007), pods/plant (Sharma *et al.* 2009) and 100 seed weight (Sharma *et al*. 2013) contributed maximum towards total genetic divergence.

Table 5 Canonical vectors showing best linear functions of varieties in pea

Characters	Vector 1	Vector 2	Vector 3
PH	0.26960	0.35982	-0.86933
DF	0.38979	0.75234	0.44968
IFP	0.05863	0.23733	-0.00607
PL	-0.08103	0.02606	0.10160
NPP	0.09424	0.09474	0.02050
TPW	-0.84016	0.43869	-0.05322
NSP	-0.09015	0.12946	0.08024
PYP	0.06903	0.02930	0.09912
SP	0.19425	-0.16875	0.11032
Canonical percentage	73.18092	13.79417	6.57513

Abbreviation of traits provided in Table 1.

Table 6 Contribution of each character to the total divergence

Characters	Number of times appearing first in ranking	Percent contribution
PH	1438	11.31
DF	3031	23.83
IFP	146	1.15
PL	9	0.07
NPP	28	0.22
TPW	7415	58.29
NSP	0	0.00
PYP	23	0.18
SP	630	4.95
Total	12720	100

Abbreviation of traits provided in Table 1.

In genetic improvement for higher yield, the choice of parent is important and desirable component characters of yield which should be taken into consideration for component breeding to obtain appropriate plant type (Mohammad *et al.* 2009). The genotypes belonging to cluster III showed the highest number of seeds/pod (7.56), 10-pod weight (95.83 g), pod length (9.02 cm), lower number of internodes for first pod (8.93) and days to 50% flowering. The maximum inter-cluster distance was noticed between III and XIV (61.49), followed by III and VII (56.58) and III and XII (53.27). This indicates that the genotypes of these clusters are much diverse to each other. The crossing among genotypes of these clusters selected for specific component traits may be helpful in bringing new gene pool and expanding the range of adaptation. Continuous selection in advance generation may lead to development of lines with high yield combining desirable component traits.

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